AMENDMENTS TO THE SPECIFICATION:

On page 1 of the specification, please replace the paragraph beginning at line 14 with the following paragraph:

Currently, there are several types of types of gene microarray technologies with arrayed DNA sequences of known identity; these include arraying cDNA on a substrate and the immobilization of oligonucleotide probes. In either version, the gene chips are exposed to DNA or RNA targets, generally single stranded, to allow for hybridization between the immobilized probe and the target. Watson-Crick DNA-DNA hybridization is the basic underlying principle for both of these microarray formats and thus native target nucleic acid is always denatured for use in these microarray formats. The DNA-DNA hybridization is a non-enzymatic mass action driven process dependent on reaction time, temperature and DNA concentration which can result in a number of hybridization reactions and artifacts, including incorrect sequence alignments due to repeat sequences in DNA. An additional problem with mass action based DNA-DNA hybridization procedures is the presence of secondary structures in single-stranded DNA substrates ~~in single-stranded DNA substrates~~ which can severely affect the hybridization process and lead to either misleading results or those that are hard to interpret. RecA protein (or its homologues such as Rad51) binds to either single-stranded DNA or RNA to form right-handed helical structures known as nucleoprotein filaments. RecA protein binds to single-stranded DNA in a cooperative manner and stretches the DNA approximately 1.5 times the length of the B-form of DNA and in the process removes the secondary structures in the single-stranded DNA or RNA. These nucleoprotein filaments rapidly catalyze the search for homology to find a homologous or partly homologous native non-denatured DNA target in a vast excess of genomic or other gene sequences. Depending on the conditions, RecA nucleoprotein filaments allow native DNA hybridization with either completely homologous DNA or with DNA containing significant heterologies (up to 30% mismatch). This is important for mutation detection and gene family detection.